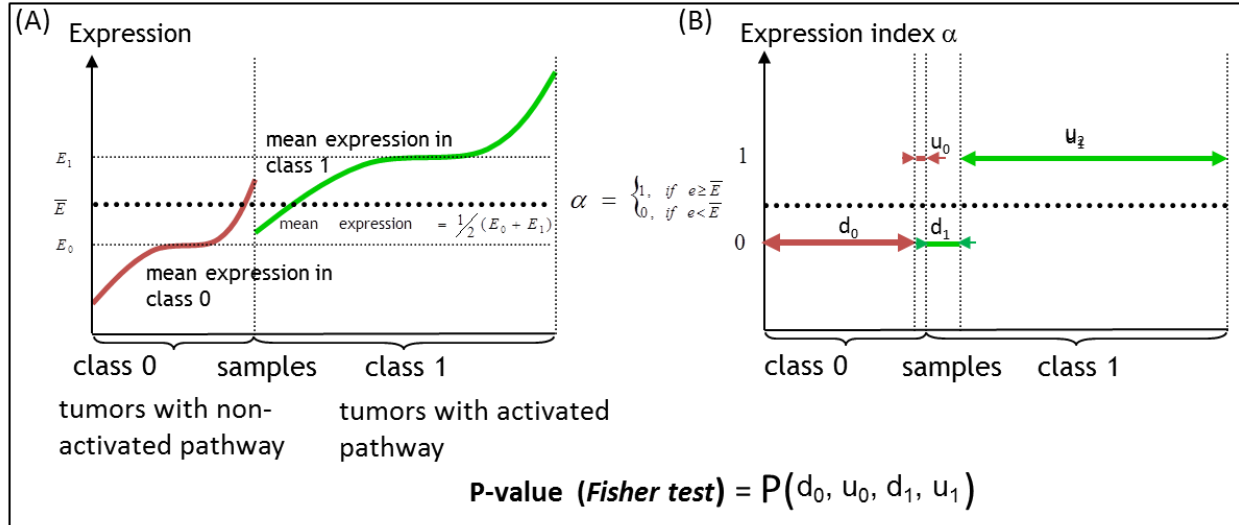


Supplementary Figure 1.



Supplementary Figure 1. Discrete approximation. (A) For each gene, the mean expression values, E_0 and E_1 , are computed for sample classes 0 and 1, respectively. The discrete approximation threshold, \bar{E} , is defined as the average value of E_0 and E_1 . (B) A discrete index “u” or “1” is assigned to an expression value e , if $e \geq \bar{E}$; an index “d” or “0” is assigned to e , if $e < \bar{E}$. Thus, depending on a gene’s expression values, samples of class 0 are separated into two groups, d_0 and u_0 , and samples of class 1 are separated into groups d_1 and u_1 , respectively. For clarity, expression values are sorted within each of the sample classes. The statistical significance of association between expression values and tumor classes is assessed by Fisher test.